



#20

1

## SEQUENCE LISTING

<110> CO, MAN SUNG  
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GRAY, GARY S.  
KNIGHT, ANDREA  
O'HARA, DENISE  
RUP, BONITA  
VELDMAN, GEERTRUIDA M.

<120> HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7 MOLECULES AND  
METHODS OF TREATMENT THEREWITH

<130> 08702.0083-00000

<140> 09/501,102  
<141> 2000-02-09

<150> 09/339,596  
<151> 1999-06-24

<150> 09/249,011  
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<170> PatentIn Ver. 2.1

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<220>  
<221> CDS  
<222> (1)..(405)

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1 5 10 15  
gtg cac tcc cag gtc cag ctg cag cag tct ggg cct gag ctg gtg agg 96  
Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Arg  
20 25 30  
cct ggg gaa tca gtg aag att tcc tgc aag ggt tcc ggc tac aca ttc 144  
Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe  
35 40 45  
act gat tat gct ata cag tgg gtg aag cag agt cat gca aag agt cta 192  
Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu  
50 55 60

gag tgg att gga gtt att aat att tac tat gat aat aca aac tac aac 240  
 Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
 65 70 75 80

cag aag ttt aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc 288  
 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser  
 85 90 95

aca gcc tat atg gaa ctt gcc aga ttg aca tct gag gat tct gcc atc 336  
 Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile  
 100 105 110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa gga 384  
 Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
 115 120 125

acc tca gtc acc gtc tcc tca 405  
 Thr Ser Val Thr Val Ser Ser  
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<210> 2  
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<400> 2  
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 Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe  
 35 40 45  
 Thr Asp Tyr Ala Ile Gln Trp Val Lys Gln Ser His Ala Lys Ser Leu  
 50 55 60  
 Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
 65 70 75 80  
 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser  
 85 90 95  
 Thr Ala Tyr Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile  
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 Thr Ser Val Thr Val Ser Ser  
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<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (1)..(396)

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1 5 10 15	
ggg acc tgt ggg gac att gtg ctg tca cag tct cca tcc tcc ctg gct	96
Gly Thr Cys Gly Asp Ile Val Leu Ser Gln Ser Pro Ser Ser Leu Ala	
20 25 30	
gtg tca gca gga gag aag gtc act atg agc tgc aaa tcc agt cag agt	144
Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser	
35 40 45	
ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag	192
Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln	
50 55 60	
aaa cca ggg cag tct cct aaa ctg ctg atc tac tgg gca tcc act agg	240
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg	
65 70 75 80	
gaa tct ggg gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat	288
Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp	
85 90 95	
ttc act ctc acc atc agc agt gtg cag gct gaa gac ctg gca gtt tat	336
Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr	
100 105 110	
tac tgc acg caa tct tat aat ctt tac acg ttc gga ggg ggg acc aag	384
Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gly Gly Thr Lys	
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Leu Glu Ile Lys	
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<211> 132

<212> PRT

<213> Mus sp.

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atg	ggg	tgg	aac	tgt	atc	atc	ttc	ttt	ctg	ggt	acc	aca	gct	aca	ggg	48
Met	Gly	Trp	Asn	Cys	Ile	Ile	Phe	Phe	Leu	Val	Thr	Thr	Ala	Thr	Gly	
1				5					10					15		
gtg	cac	tcc	cag	gtc	cag	ctg	gtg	cag	tct	ggg	gct	gag	gtg	aag	aag	96
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
			20					25					30			
cct	ggg	agc	tca	gtg	aag	gtg	tcc	tgc	aaa	gct	tcc	ggc	tac	aca	ttc	144
Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
		35					40					45				
act	gat	tat	gct	ata	cag	tgg	gtg	aga	cag	gct	cct	gga	cag	ggc	ctc	192
Thr	Asp	Tyr	Ala	Ile	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
	50					55					60					
gag	tgg	att	gga	gtt	att	aat	att	tac	tat	gat	aat	aca	aac	tac	aac	240
Glu	Trp	Ile	Gly	Val	Ile	Asn	Ile	Tyr	Tyr	Asp	Asn	Thr	Asn	Tyr	Asn	
65					70					75					80	

cag aag ttt aag ggc aag gcc aca atg act gta gac aag tcg acg agc 288  
 Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
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aca gcc tat atg gaa ctt agt tct ttg aga tct gag gat acg gcc gtt 336  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
                   100                                  105                                  110

tat tac tgt gca aga gcg gcc tgg tat atg gac tac tgg ggt caa ggt 384  
 Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
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acc ctt gtc acc gtc tcc tca 405  
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<210> 6

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 peptide sequence

<400> 6

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Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
                   20                                  25                                  30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
                   35                                  40                                  45

Thr Asp Tyr Ala Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
                   50                                  55                                  60

Glu Trp Ile Gly Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn  
                   65                                  70                                  75                                  80

Gln Lys Phe Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Thr Ser  
                   85                                  90                                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
                   100                                  105                                  110

Tyr Tyr Cys Ala Arg Ala Ala Trp Tyr Met Asp Tyr Trp Gly Gln Gly  
                   115                                  120                                  125

Thr Leu Val Thr Val Ser Ser  
                   130                                  135

<210> 7

<211> 396

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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<220>

<221> CDS

<222> (1)..(396)

<400> 7

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1 5 10 15	
ggc acc tgt ggg gac att gtg ctg aca cag tct cca gat tcc ctg gct	96
Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala	
20 25 30	
gta agc tta gga gag agg gcc act att agc tgc aaa tcc agt cag agt	144
Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser	
35 40 45	
ctg ctc aac agt aga acc cga gag aac tac ttg gct tgg tac cag cag	192
Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln	
50 55 60	
aaa cca ggg cag cct cct aaa ctg ctg atc tac tgg gca tcc act agg	240
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg	
65 70 75 80	
gaa tct ggg gtc cct gat cgc ttc agt ggc agt gga tct ggg aca gat	288
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
85 90 95	
ttc act ctc acc atc agc agt ctg cag gct gaa gac gtg gca gtt tat	336
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr	
100 105 110	
tac tgc acg caa tct tat aat ctt tac acg ttc gga cag ggg acc aag	384
Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys	
115 120 125	
gtg gaa ata aaa	396
Val Glu Ile Lys	
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<210> 8

<211> 132

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
peptide sequence

&lt;400&gt; 8

Met Asp Ser Gln Ala Gln Val Leu Ile Leu Leu Leu Leu Trp Val Ser  
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Gly Thr Cys Gly Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala  
 20 25 30

Val Ser Leu Gly Glu Arg Ala Thr Ile Ser Cys Lys Ser Ser Gln Ser  
 35 40 45

Leu Leu Asn Ser Arg Thr Arg Glu Asn Tyr Leu Ala Trp Tyr Gln Gln  
 50 55 60

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
 65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 85 90 95

Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr  
 100 105 110

Tyr Cys Thr Gln Ser Tyr Asn Leu Tyr Thr Phe Gly Gln Gly Thr Lys  
 115 120 125

Val Glu Ile Lys  
 130

&lt;210&gt; 9

&lt;211&gt; 15

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic nucleotide sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(15)

&lt;400&gt; 9

gat tat gct ata cag  
 Asp Tyr Ala Ile Gln  
 1 5

15

&lt;210&gt; 10

&lt;211&gt; 5

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic peptide sequence

<400> 10  
 Asp Tyr Ala Ile Gln  
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<210> 11  
 <211> 51  
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 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (1)..(51)

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 1 5 10 15

ggc 51  
 Gly

<210> 12  
 <211> 17  
 <212> PRT  
 <213> Mus sp.

<400> 12  
 Val Ile Asn Ile Tyr Tyr Asp Asn Thr Asn Tyr Asn Gln Lys Phe Lys  
 1 5 10 15

Gly

<210> 13  
 <211> 21  
 <212> DNA  
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 <222> (1)..(21)

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 Ala Ala Trp Tyr Met Asp Tyr  
 1 5

<210> 14  
 <211> 7  
 <212> PRT  
 <213> Mus sp.



&lt;400&gt; 14

Ala Ala Trp Tyr Met Asp Tyr  
1 5

&lt;210&gt; 15

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(51)

&lt;400&gt; 15

aaa	tcc	agt	cag	agt	ctg	ctc	aac	agt	aga	acc	cga	gag	aac	tac	ttg	48
Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Ser	Arg	Thr	Arg	Glu	Asn	Tyr	Leu	
1					5				10					15		

gct

51

Ala

&lt;210&gt; 16

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Mus sp.

&lt;400&gt; 16

Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asn	Ser	Arg	Thr	Arg	Glu	Asn	Tyr	Leu
1					5				10					15	

Ala

&lt;210&gt; 17

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(21)

&lt;400&gt; 17

tgg	gca	tcc	act	agg	gaa	tct	
Trp	Ala	Ser	Thr	Arg	Glu	Ser	21
1				5			

&lt;210&gt; 18

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Mus sp.

&lt;400&gt; 18

Trp Ala Ser Thr Arg Glu Ser  
 1 5

&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(24)

&lt;400&gt; 19

acg caa tct tat aat ctt tac acg  
 Thr Gln Ser Tyr Asn Leu Tyr Thr  
 1 5

24

&lt;210&gt; 20

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Mus sp.

&lt;400&gt; 20

Thr Gln Ser Tyr Asn Leu Tyr Thr  
 1 5

&lt;210&gt; 21

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(405)

&lt;400&gt; 21

atg aaa tgc agc tgg gtc atc ttc ttc ctg atg gca gtg gtt aca ggg 48  
 Met Lys Cys Ser Trp Val Ile Phe Phe Leu Met Ala Val Val Thr Gly  
 1 5 10 15

gtc aat tca gag gtt cac ctg cag cag tct ggg gct gag ctt gtg agg 96  
 Val Asn Ser Glu Val His Leu Gln Gln Ser Gly Ala Glu Leu Val Arg  
 20 25 30

cca ggg gcc tta gtc aag ttg tcc tgc aaa cct tct ggc ttc aac att 144  
 Pro Gly Ala Leu Val Lys Leu Ser Cys Lys Pro Ser Gly Phe Asn Ile  
 35 40 45

aaa gac tac tat atg cac tgg gtg aag cag agg cct gaa cag ggc ctg 192  
 Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu  
 50 55 60

gag tgg att gga tgg att gat cct gag aat ggt aat act cta tat gac 240  
 Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Leu Tyr Asp  
     65                    70                    75                    80

ccg aag ttc cag ggc aag gcc agt ata aca gca gac aca tcc tcc aac 288  
 Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ala Asp Thr Ser Ser Asn  
                     85                    90                    95

aca gcc tac ctg cag ctc agc agc ctg aca tct gag gac act gcc gtc 336  
 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val  
                     100                    105                    110

tat tac tgt gct aga gag ggg ctt ttt ttt gct tac tgg ggc caa ggg 384  
 Tyr Tyr Cys Ala Arg Glu Gly Leu Phe Phe Ala Tyr Trp Gly Gln Gly  
             115                    120                    125

act ccg gtc act gtc tct gca 405  
 Thr Pro Val Thr Val Ser Ala  
     130                    135

<210> 22  
 <211> 135  
 <212> PRT  
 <213> Mus sp.

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             20                    25                    30  
 Pro Gly Ala Leu Val Lys Leu Ser Cys Lys Pro Ser Gly Phe Asn Ile  
             35                    40                    45  
 Lys Asp Tyr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu  
     50                    55                    60  
 Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Leu Tyr Asp  
     65                    70                    75                    80  
 Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ala Asp Thr Ser Ser Asn  
                     85                    90                    95  
 Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val  
     100                    105                    110  
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     115                    120                    125  
 Thr Pro Val Thr Val Ser Ala  
     130                    135

<210> 23  
 <211> 390

&lt;212&gt; DNA

&lt;213&gt; Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(390)

&lt;400&gt; 23

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atg gat ttt cat gtg cag att ttc agc ttc atg cta atc agt gtc aca 48
Met Asp Phe His Val Gln Ile Phe Ser Phe Met Leu Ile Ser Val Thr
  1             5             10             15

gtc ata ttg tcc agt gga gaa att gtg ctc acc cag tct cca gca ctc 96
Val Ile Leu Ser Ser Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Leu
             20             25             30

atg gct gca tct cca ggg gag aag gtc acc atc acc tgc agt gtc agc 144
Met Ala Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Val Ser
             35             40             45

tca agt ata agt tcc agc aac ttg cac tgg tac cag cag aag tca gaa 192
Ser Ser Ile Ser Ser Ser Asn Leu His Trp Tyr Gln Gln Lys Ser Glu
             50             55             60

acc tcc ccc aaa ccc tgg att tat ggc aca tcc aac ctg gct tct gga 240
Thr Ser Pro Lys Pro Trp Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly
             65             70             75             80

gtc cct gtt cgc ttc agt ggc agt gga tct ggg acc tct tat tct ctc 288
Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
             85             90             95

aca atc agc agc atg gag gct gaa gat gct gcc act tat tac tgt caa 336
Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln
             100            105            110

cag tgg agt agt tac cca ctc acg ttc ggt gct ggg acc aag ctg gag 384
Gln Trp Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
             115            120            125

ctg aaa 390
Leu Lys
  130

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&lt;210&gt; 24

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Mus sp.

&lt;400&gt; 24

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Met Asp Phe His Val Gln Ile Phe Ser Phe Met Leu Ile Ser Val Thr
  1             5             10             15

Val Ile Leu Ser Ser Gly Glu Ile Val Leu Thr Gln Ser Pro Ala Leu
             20             25             30

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atg	aaa	tgc	agc	tgg	gtc	atc	ttc	ttc	ctg	atg	gca	gtg	gtt	aca	ggg	48
Met	Lys	Cys	Ser	Trp	Val	Ile	Phe	Phe	Leu	Met	Ala	Val	Val	Thr	Gly	
1				5					10					15		
gtc	aat	tca	gag	gtt	cag	ctg	gtg	cag	tct	ggg	gct	gag	gtt	aag	aag	96
Val	Asn	Ser	Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
			20					25					30			
cca	ggg	gcc	tca	gtc	aag	gtg	tcc	tgc	aaa	cct	tct	ggc	ttc	aac	att	144
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Pro	Ser	Gly	Phe	Asn	Ile	
		35					40					45				
aaa	gac	tac	tat	atg	cac	tgg	gtg	agg	cag	gcg	cct	gga	cag	ggc	ctc	192
Lys	Asp	Tyr	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
	50					55					60					
gag	tgg	att	gga	tgg	att	gat	cct	gag	aat	ggg	aat	act	cta	tat	gac	240
Glu	Trp	Ile	Gly	Trp	Ile	Asp	Pro	Glu	Asn	Gly	Asn	Thr	Leu	Tyr	Asp	
65					70					75					80	

ccg aag ttc cag ggc aag gcc act ata act gca gac aca tcc acc agc 288  
 Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Thr Ser  
                   85                                  90                                  95

aca gcc tac atg gag ctg agc agc ctg aga tct gag gac act gcc gtc 336  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
                   100                                  105                                  110

tat tac tgt gct aga gag ggg ctt ttt ttt gct tac tgg ggc caa ggt 384  
 Tyr Tyr Cys Ala Arg Glu Gly Leu Phe Phe Ala Tyr Trp Gly Gln Gly  
                   115                                  120                                  125

acc ctg gtc act gtc tct tca 405  
 Thr Leu Val Thr Val Ser Ser  
                   130                                  135

<210> 26

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 peptide sequence

<400> 26

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Val Asn Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
                   20                                  25                                  30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Pro Ser Gly Phe Asn Ile  
                   35                                  40                                  45

Lys Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
                   50                                  55                                  60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Gly Asn Thr Leu Tyr Asp  
                   65                                  70                                  75                                  80

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Thr Ser  
                   85                                  90                                  95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
                   100                                  105                                  110

Tyr Tyr Cys Ala Arg Glu Gly Leu Phe Phe Ala Tyr Trp Gly Gln Gly  
                   115                                  120                                  125

Thr Leu Val Thr Val Ser Ser  
                   130                                  135

<210> 27

<211> 390

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
nucleotide sequence

<220>

<221> CDS

<222> (1)..(390)

<400> 27

atg gat ttt cat gtg cag att ttc agc ttc atg cta atc agt gtc aca	48
Met Asp Phe His Val Gln Ile Phe Ser Phe Met Leu Ile Ser Val Thr	
1 5 10 15	
gtc ata ttg tcc agt gga gat att cag atg acc cag tct cca tca tcc	96
Val Ile Leu Ser Ser Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser	
20 25 30	
ctg tct gca tct gta ggg gat agg gtc acc atc acc tgc agt gtc agc	144
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Val Ser	
35 40 45	
tca agt ata agt tcc agc aac ttg cac tgg tac cag cag aag cca ggc	192
Ser Ser Ile Ser Ser Ser Asn Leu His Trp Tyr Gln Gln Lys Pro Gly	
50 55 60	
aag gcc ccc aaa ccc ttg att tat ggc aca tcc aac ctg gct tct gga	240
Lys Ala Pro Lys Pro Leu Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly	
65 70 75 80	
gtc cct agt cgc ttc agt ggc agt gga tct ggg acc gat tat act ctc	288
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu	
85 90 95	
aca atc agc agc ttg cag cct gaa gat gtt gcc act tat tac tgt caa	336
Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln	
100 105 110	
cag tgg agt agt tac cca ctc acg ttc ggt caa ggg acc aag gtg gag	384
Gln Trp Ser Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu	
115 120 125	
atc aaa	390
Ile Lys	
130	

<210> 28

<211> 130

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
peptide sequence

&lt;400&gt; 28

Met Asp Phe His Val Gln Ile Phe Ser Phe Met Leu Ile Ser Val Thr  
 1 5 10 15

Val Ile Leu Ser Ser Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 20 25 30

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Val Ser  
 35 40 45

Ser Ser Ile Ser Ser Ser Asn Leu His Trp Tyr Gln Gln Lys Pro Gly  
 50 55 60

Lys Ala Pro Lys Pro Leu Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly  
 65 70 75 80

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu  
 85 90 95

Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gln  
 100 105 110

Gln Trp Ser Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu  
 115 120 125

Ile Lys  
 130

&lt;210&gt; 29

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Mus sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(36)

&lt;400&gt; 29

agt gtc agc tca agt ata agt tcc agc aac ttg cac  
 Ser Val Ser Ser Ser Ile Ser Ser Ser Asn Leu His  
 1 5 10

36

&lt;210&gt; 30

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Mus sp.

&lt;400&gt; 30

Ser Val Ser Ser Ser Ile Ser Ser Ser Asn Leu His  
 1 5 10

&lt;210&gt; 31

&lt;211&gt; 21



<212> DNA  
 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (1)..(21)

<400> 31  
 ggc aca tcc aac ctg gct tct  
 Gly Thr Ser Asn Leu Ala Ser  
     1                    5

21

<210> 32  
 <211> 7  
 <212> PRT  
 <213> Mus sp.

<400> 32  
 Gly Thr Ser Asn Leu Ala Ser  
     1                    5

<210> 33  
 <211> 27  
 <212> DNA  
 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (1)..(27)

<400> 33  
 caa cag tgg agt agt tac cca ctc acg  
 Gln Gln Trp Ser Ser Tyr Pro Leu Thr  
     1                    5

27

<210> 34  
 <211> 9  
 <212> PRT  
 <213> Mus sp.

<400> 34  
 Gln Gln Trp Ser Ser Tyr Pro Leu Thr  
     1                    5

<210> 35  
 <211> 15  
 <212> DNA  
 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (1)..(15)

<400> 35  
 gac tac tat atg cac  
 Asp Tyr Tyr Met His  
     1                    5

15

<210> 36  
 <211> 5  
 <212> PRT  
 <213> Mus sp.

<400> 36  
 Asp Tyr Tyr Met His  
     1                    5

<210> 37  
 <211> 51  
 <212> DNA  
 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (1)..(51)

<400> 37  
 tgg att gat cct gag aat ggt aat act cta tat gac ccg aag ttc cag 48  
 Trp Ile Asp Pro Glu Asn Gly Asn Thr Leu Tyr Asp Pro Lys Phe Gln  
     1                    5                    10                    15

ggc 51  
 Gly

<210> 38  
 <211> 17  
 <212> PRT  
 <213> Mus sp.

<400> 38  
 Trp Ile Asp Pro Glu Asn Gly Asn Thr Leu Tyr Asp Pro Lys Phe Gln  
     1                    5                    10                    15

Gly

<210> 39  
 <211> 21  
 <212> DNA  
 <213> Mus sp.

<220>  
 <221> CDS  
 <222> (1)..(21)

<400> 39  
gag ggg ctt ttt ttt gct tac  
Glu Gly Leu Phe Phe Ala Tyr  
1 5

21

<210> 40  
<211> 7  
<212> PRT  
<213> Mus sp.

<400> 40  
Glu Gly Leu Phe Phe Ala Tyr  
1 5